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TABLE 1

<u>M</u> PPKTPRKTAATAAAAAAEPAPPPPPPPPEEDPE	( 34 )
QDSGPEDLPLVRLEFEETEEPDTALCQKLKIPDHVRERA	( 74 )
WLTWEKVSSVDGVLGGYIQKKKELWGICIFIAAVDLDE <u>M</u> S	( 114 )
FTFTELQKNIEISVHKFFNLLKEIDTSTKVDNAMSRLKK	( 154 )
YDVLFAFLSKLERTCELIYLTQPSSSISTEINSALVLKVS	( 194 )
WITFLAKGEVLQMEDDLVISFQLNLCVLDYFIKLSPPML	( 234 )
LKEPYKTAVIPINGSRPTPRRGQMRSARIAKQLENDTRII	( 274 )
EVLCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEV	( 314 )
ENLSKRYEEIYLKNKDLDARLFLDHDKTLQTDSIDSFETQ	( 354 )
RTPRKSNLDEEVNVI PPHTPVRTVMNTIQQLMILNSASD	( 394 )
QPSENLISYFNNCTVNPKESILKRVKDIGYIFKEKFAKAV	( 434 )
GQGCVEIGSQRYKLGVRLYYRVMESMLKSEEERLSIQNFS	( 474 )
KLLNDNIFHMSLLACALEVVMATYSRSTSQNLD SGTDLSF	( 514 )
PWILNVNLNKA FDFYKVIESFIKAEGNLTREMIKHLERCE	( 554 )
HRIMESLAWLSDSPLFDLIKQSKDREGPTDHLESACPLNL	( 594 )
PLQNNHTAADMYLSPVRSPKKKGSTTRVNSTANAETQATS	( 634 )
AFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHP	( 674 )
ELEHIIWTLFQHTLQNEYELMRDRHLDQIMMCSMYGICKV	( 714 )
KNIDLKFKIIIVTAYKDLPHAVQETFKRVLIKEEEYDSIIV	( 754 )
FYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFPS	( 794 )
SPLRIPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVS	( 834 )
IGESFGTSEKFQKINQMVCNSDRVLKRSAEGSNPPKPLKK	( 874 )
LRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMQKQ	( 914 )
KMNDSMDTSNKEEK	( 928 )

single-letter abbreviations for the amino acid residues are:

A, Ala; C, Cys; D, Asp; E, Gly; F, Phe; G, Gly; H, His;  
 I, Ile; K, Lys; L, Leu; M, Met; N, Asn; P, Pro; Q, Gln;  
 R, Arg; S, Ser; T, Thr; V, Val; W, Trp; and Y, Tyr.--

Please replace paragraph [153] beginning at page 27, line 15, with the following:

[153] --The amino acid sequence (Table 1; SEQ ID NO:2) is written in the abbreviation code recognized in the art. Single-letter abbreviations for the amino acid residues are: A = Alanine, C = Cysteine, D = Aspartic acid, E = Glutamic Acid, F = Phenylalanine, G = Glycine, H = Histidine, I = Isoleucine, K = Lysine, L = Leucine, M = Methionine, N =

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Asparagine, P = Proline, Q = Glutamine, R = Arginine, S = Serine, T = Threonine, V = Valine, W = Tryptophane and Y = Tyrosine.--

Please replace paragraph [225] beginning at page 27, line 15, with the following:

[225] --Pending U.S. patent application Serial No. 108,748 discloses and claims the RB gene and its clone. The RB gene and its clone had the nucleotide and amino acid sequences ~~sequence~~ depicted in Table 4 ~~Table 2~~ (SEQ ID NOS:1 and 2).

TABLE 4

TTCCGGTTTT TCTCAGGGGA CGTTGAAATT ATTTTGTAA CGGGAGTCGG GAGAGGACGG	60
GGCGTGCCCC GCGTGC GCGC GCGTCGTCCT CCCC GCGCT CCTCCACAGC TCGCTGGCTC	120
CCGCCGCGGA AAGGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC	171
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala	
1 5 10	
ACC GCC GCC GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC	219
Thr Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro	
15 20 25	
CCT CCT GAG GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT	267
Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro	
30 35 40	
CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA	315
Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala	
45 50 55	
TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG	363
Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp	
60 65 70 75	
TTA ACT TGG GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT	411
Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr	
80 85 90	
ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA	459
Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala	
95 100 105	
GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC	507
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn	
110 115 120	

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ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT	555
Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp	
125 130 135	
ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT	603
Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr	
140 145 150 155	
GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT	651
Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu	
160 165 170	
ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT	699
Ile Tyr Leu Thr Gln Pro Ser Ser Ile Ser Thr Glu Ile Asn Ser	
175 180 185	
GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG	747
Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly	
190 195 200	
GAA GTA TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG	795
Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met	
205 210 215	
CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC	843
Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu	
220 225 230 235	
AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA	891
Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg	
240 245 250	
ACA CCC AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA	939
Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu	
255 260 265	
GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT	987
Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys	
270 275 280	
AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT	1035
Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe	
285 290 295	
ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA	1083
Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu	
300 305 310 315	
AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA	1131
Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu	
320 325 330	

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GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT	1179
Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser	
335 340 345	
ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT	1227
Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp	
350 355 360	
GAA GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG	1275
Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met	
365 370 375	
AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA	1323
Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln	
380 385 390 395	
CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA	1371
Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro	
400 405 410	
AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA	1419
Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys	
415 420 425	
GAG AAA TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA	1467
Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser	
430 435 440	
CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC	1515
Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser	
445 450 455	
ATG CTT AAA TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA	1563
Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys	
460 465 470 475	
CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT	1611
Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu	
480 485 490	
GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT	1659
Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp	
495 500 505	
TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA	1707
Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu	
510 515 520	
AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA	1755
Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu	
525 530 535	

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GGC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT	1803
Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His	
540 545 550 555	
CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT	1851
Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp	
560 565 570	
CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA	1899
Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu	
575 580 585	
TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA	1947
Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala	
590 595 600	
GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT	1995
Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr	
605 610 615	
ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC	2043
Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala	
620 625 630 635	
TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT	2091
Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr	
640 645 650	
AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA	2139
Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu	
655 660 665	
CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT	2187
Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu	
670 675 680	
TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT	2235
Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His	
685 690 695	
TTG GAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG	2283
Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys	
700 705 710 715	
AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT	2331
Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu	
720 725 730	
CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG	2379
Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu	
735 740 745	
GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA	2427

Glu	Tyr	Asp	Ser	Ile	Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg		
750						755						760					
CTG	AAA	ACA	AAT	ATT	TTG	CAG	TAT	GCT	TCC	ACC	AGG	CCC	CCT	ACC	TTG	2475	
Leu	Lys	Thr	Asn	Ile	Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu		
765						770						775					
TCA	CCA	ATA	CCT	CAC	ATT	CCT	CGA	AGC	CCT	TAC	AAG	TTT	CCT	AGT	TCA	2523	
Ser	Pro	Ile	Pro	His	Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser		
780						785						790					795
CCC	TTA	CGG	ATT	CCT	GGA	GGG	AAC	ATC	TAT	ATT	TCA	CCC	CTG	AAG	AGT	2571	
Pro	Leu	Arg	Ile	Pro	Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser		
800						805						810					
CCA	TAT	AAA	ATT	TCA	GAA	GGT	CTG	CCA	ACA	CCA	ACA	AAA	ATG	ACT	CCA	2619	
Pro	Tyr	Lys	Ile	Ser	Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro		
815						820						825					
AGA	TCA	AGA	ATC	TTA	GTA	TCA	ATT	GGT	GAA	TCA	TTC	GGG	ACT	TCT	GAG	2667	
Arg	Ser	Arg	Ile	Leu	Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu		
830						835						840					
AAG	TTC	CAG	AAA	ATA	AAT	CAG	ATG	GTA	TGT	AAC	AGC	GAC	CGT	GTG	CTC	2715	
Lys	Phe	Gln	Lys	Ile	Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu		
845						850						855					
AAA	AGA	AGT	GCT	GAA	GGA	AGC	AAC	CCT	CCT	AAA	CCA	CTG	AAA	AAA	CTA	2763	
Lys	Arg	Ser	Ala	Glu	Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu		
860						865						870					875
CGC	TTT	GAT	ATT	GAA	GGA	TCA	GAT	GAA	GCA	GAT	GGA	AGT	AAA	CAT	CTC	2811	
Arg	Phe	Asp	Ile	Glu	Gly	Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	His	Leu		
880						885						890					
CCA	GGA	GAG	TCC	AAA	TTT	CAG	CAG	AAA	CTG	GCA	GAA	ATG	ACT	TCT	ACT	2859	
Pro	Gly	Glu	Ser	Lys	Phe	Gln	Gln	Lys	Leu	Ala	Glu	Met	Thr	Ser	Thr		
895						900						905					
CGA	ACA	CGA	ATG	CAA	AAG	CAG	AAA	ATG	AAT	GAT	AGC	ATG	GAT	ACC	TCA	2907	
Arg	Thr	Arg	Met	Gln	Lys	Gln	Lys	Met	Asn	Asp	Ser	Met	Asp	Thr	Ser		
910						915						920					
AAC	AAG	GAA	GAG	AAA	TGAGGATCTC	AGGACCTTGG	TGGACACTGT	GTACACCTCT								2962	
Asn	Lys	Glu	Glu	Lys													
925																	
GGATTCATTG TCTCTCACAG ATGTGACTGT AT																2994	

TABLE 4

TTCCGGTTTT TCTCAGGGGA CGTTGAAATT ATTTTTGTAA CCGGAGTCGG GACAGGACCG	60
GGCGTGCCCC GCGTGCGCGC GCGTCGTCCT CCCCCGCGCT CCTCCACAGC TCGCTGGCTC	120
CCGCGCGCGA AACGCGTC ATC CCG CCC AAA ACC CCC CCA AAA ACG CCC GCC	171
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala	
1 5 10	
ACC GCC GCC GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC	219
Thr Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro	
15 20 25	
CCT CCG TAG GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTC CCT	267
Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro	
30 35 40	
CTC GTC ACG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA	315
Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala	
45 50 55	
TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC ACA GAG ACA GCT TCG	363
Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp	
60 65 70 75	
TTA ACT TCG CAG AAA GTT TCA TCT CTG GAT GGA GTA TTG CCA GGT TAT	411
Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr	
80 85 90	
ATT CAA AAG AAA AAG GAA CTG TGG CGA ATC TGT ATC TTT ATT GCA GCA	459
Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala	
95 100 105	
GTT CAC CTA GAT CAG ATC TCG TTC ACT TTT ACT CAG CTA CAG AAA AAC	507
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn	
110 115 120	
ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT	555
Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp	
125 130 135	
ACC AGT ACC AAA GTT CAT AAT GCT ATG TCA ACA CTG TTC AAG AAG TAT	603
Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr	
140 145 150 155	
GAT GTA TTG TTT CCA CTC TTC ACC AAA TTG CAA ACG ACA TGT GAA CTT	651
Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu	
160 165 170	



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ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT 699  
 Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser  
 175 180 185

GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG 747  
 Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly  
 190 195 200

GAA GTA TTA CAA ATC GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATC 795  
 Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met  
 205 210 215

CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC 843  
 Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu  
 220 225 230 235

AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA 891  
 Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg  
 240 245 250

ACA CCC AGC CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA 939  
 Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu  
 255 260 265

GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT 987  
 Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys  
 270 275 280

AAT ATA GAT CAG CTC AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT 1035  
 Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe  
 285 290 295

ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GCA CTT CCA GAG GTT GAA 1083  
 Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu  
 300 305 310 315

AAT CTT TCT AAA CGA TAC CAA GAA ATT TAT CTT AAA AAT AAA GAT CTA 1131  
 Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu  
 320 325 330

GAT GCA ACA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT 1179  
 Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser  
 335 340 345

ATA GAC AGT TTT GAA ACA CAG ACA ACA CCA CGA AAA AGT AAC CTT GAT 1227  
 Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp  
 350 355 360

GAA GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG 1275  
 Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met  
 365 370 375

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~~AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA~~ 1323  
~~Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln~~  
~~380 385 390 395~~

~~CCT TCA GAA AAT CTC ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA~~ 1371  
~~Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro~~  
~~400 405 410~~

~~AAA GAA AGT ATA CTC AAA ACA GTG AAG GAT ATA CGA TAC ATC TTT AAA~~ 1419  
~~Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys~~  
~~415 420 425~~

~~GAG AAA TTT GCT AAA GCT CTC GCA CAG CCT TCT GTC CAA ATT GCA TCA~~ 1467  
~~Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser~~  
~~430 435 440~~

~~CAG CGA TAC AAA CTT GCA GTT CCC TTG TAT TAC CGA GTA ATG GAA TCC~~ 1515  
~~Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser~~  
~~445 450 455~~

~~ATC CTT AAA TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA~~ 1563  
~~Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys~~  
~~460 465 470 475~~

~~CTT CTC AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT~~ 1611  
~~Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu~~  
~~480 485 490~~

~~GAG GTT GTA ATG GCC ACA TAT AGC ACA AGT ACA TCT CAG AAT CTT GAT~~ 1659  
~~Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp~~  
~~495 500 505~~

~~TCT GCA ACA CAT TTG TCT TTC CCA TGG ATT CTC AAT GTC CTT AAT TTA~~ 1707  
~~Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu~~  
~~510 515 520~~

~~AAA GCC TTT CAT TTT TAC AAA CTG ATC GAA AGT TTT ATC AAA GCA GAA~~ 1755  
~~Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu~~  
~~525 530 535~~

~~GGC AAC TTG ACA ACA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT~~ 1803  
~~Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His~~  
~~540 545 550 555~~

~~CGA ATC ATG CAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT~~ 1851  
~~Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp~~  
~~560 565 570~~

~~CTT ATT AAA CAA TCA AAG GAC CGA GAA GCA CCA ACT CAT CAC CTT GAA~~ 1899  
~~Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu~~  
~~575 580 585~~

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TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA — 1947  
 Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala  
 — 590 — 595 — 600

GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT — 1995  
 Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr  
 — 605 — 610 — 615

ACG CGT GTA AAT TCT ACT GCA AAT GCA CAG ACA CAA GCA ACC TCA GCC — 2043  
 Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala  
 620 — 625 — 630 — 635

TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT — 2091  
 Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr  
 — 640 — 645 — 650

AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA — 2139  
 Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu  
 — 655 — 660 — 665

CGC CTT CTG TCT CAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT — 2187  
 Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu  
 — 670 — 675 — 680

TTC CAG CAC ACC CTG CAG AAT CAG TAT GAA CTC ATG ACA GAC AGG CAT — 2235  
 Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His  
 — 685 — 690 — 695

TTC CAG CAA ATT ATG ATG TGT TCC ATG TAT GCC ATA TGC AAA GTG AAG — 2283  
 Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys  
 700 — 705 — 710 — 715

AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT — 2331  
 Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu  
 — 720 — 725 — 730

CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT GTT TTC ATC AAA GAA GAG — 2379  
 Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu  
 — 735 — 740 — 745

GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG ACA — 2427  
 Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg  
 — 750 — 755 — 760

CTG AAA ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG — 2475  
 Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu  
 — 765 — 770 — 775

TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT ACT TCA — 2523  
 Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser  
 780 — 785 — 790 — 795

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~~CCC TTA CGG ATT CCT GCA GCG AAC ATC TAT ATT TCA CCC CTG AAG AGT~~ 2571  
~~Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser~~  
 800 805 810

~~CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA~~ 2619  
~~Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro~~  
 815 820 825

~~AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GCG ACT TCT GAG~~ 2667  
~~Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu~~  
 830 835 840

~~AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTC CTC~~ 2715  
~~Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu~~  
 845 850 855

~~AAA AGA AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA~~ 2763  
~~Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu~~  
 860 865 870 875

~~CGC TTT CAT ATT CAA CGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC~~ 2811  
~~Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu~~  
 880 885 890

~~CCA GGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT~~ 2859  
~~Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr~~  
 895 900 905

~~CGA ACA CCA ATG CAA AAG CAG AAA ATG AAT CAT AGC ATG CAT ACC TCA~~ 2907  
~~Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser~~  
 910 915 920

~~AAC AAG GAA GAG AAA TCAGCATCTC AGGACCTTGG TGGACACTGT GTACACCTCT~~ 2962  
~~Asn Lys Glu Glu Lys~~  
 925

~~GCATTCATTG TCTCTCACAG ATCTCACTGT AT~~ 2994

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Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 10, at the end of the application.